

Figure 1A

1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAGTTGTGCCAGAAAATTATGGT 60

61 TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGA 120

121 GATCTGGCAGCTCTGTGTATTTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA 180

181 AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCATGTGAGCTTGATG 240

241 GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC 300

301 CATCCAGGGTTTAAACTACTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG 360

361 ATTTCTTGGGGGAAAAATACTGGGATAAGAGGAGGTCATTTTTTAATAAGTTAGCATCCT 420

421 TTTCCCTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT 480

481 TAAATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAACTGTAGTCG 540
1 M A L S G N C S R 9

541 TTATTATCCTCGAGAACAAGGGTCCGCAGTTCCCAACTCCTTCCCTGAGGTGGTAGAGCT 600
10 Y Y P R E Q G S A V P N S F P E V V E L 29

601 GAATGTCGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC 660
30 N V G G Q V Y F T R H S T L I S I P H S 49

661 CCTCCTGTGGAAAATGTTTTCCCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC 720
50 L L W K M F S P K R D T A N D L A K D S 69

721 CAAGGGAAGGTTTTTCATTGACAGAGATGGATTCTTGTTCGGTTATATTCTGGACTATCT 780
70 K G R F F I D R D G F L F R Y I L D Y L 89

781 CAGGGACAGGCAGGTGGTCTGCCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAGGGA 840
90 R D R Q V V L P D H F P E K G R L K R E 109

841 AGCTGAATACTTCCAGCTCCAGACTTGGTCAAACCTGACCCCCGATGAAATCAAGCA 900
110 A E Y F Q L P D L V K L L T P D E I K Q 129

901 AAGCCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAG 960
130 S P D E F C H S D F E D A S Q G S D T R 149

961 AATCTGCCCCCTTCCCTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGG 1020
150 I C P P S S L L P A D R K W G F I T V G 169

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Figure 1B

1021	TTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGT	1080
170	Y R G S C T L G R E G Q A D A K F R R V	189
1081	TCCCCGGATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAAGAAGTCTTTGGAGAACTTT	1140
190	P R I L V C G R I S L A K E V F G E T L	209
1141	GAATGAAAGCAGAGACCCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAA	1200
210	N E S R D P D R A P E R Y T S R F Y L K	229
1201	ATTCAAGCACCTGGAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGC	1260
230	F K H L E R A F D M L S E <u>C G F H M V A</u>	249
1261	CTGTAACCTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC	1320
250	<u>C N S S V T A S F I N Q Y T</u> D D K I W S	269
1321	AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCACACTGCGA	1380
270	S Y T E Y V F Y R E P S R W S P S H C D	289
1381	TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGA	1440
290	C C C K N G K G D K E G E S G T S C N D	309
1441	CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT	1500
310	L S T S S C D S Q S E A S S P Q E T V I	329
1501	CTGTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG	1560
330	C G P V T R Q T N I Q T L D R P I K K G	349
1561	CCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAGCGACTTACTCCGGATTCT	1620
350	P V Q L I Q Q S E M R R K S D L L R I L	369
1621	GACTTCAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAAAAGCTGTTAAAGAAAAGCT	1680
370	T S G S R E S N M S S K K K A V K E K L	389
1681	CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCCCTAAAAAAAAAAATTCCAGA	1740
390	S I E E E L E K C I Q D F L K K K I P D	409
1741	TCGGTTTCTTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATA	1800
410	R F P E R K H P W Q S E L L R K Y H L	428
1801	AGGGAGGGCTGGGGGCGGGGAAAAAAAAAAAAAAGAGTCATTTTGAAATTAACCTCATAA	1860
1861	AAGGAATTCATATTTTAAAGGAAAAAAATACAATAATGATGCACATTCTTAGAACACA	1920
1921	ATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTACCTTAACATGTAAATCCACA	1980

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Figure 1C

1981 GGGTAGATTTCTTTCTAGATGTGGAAGTACAAGAAAATCTTTTCTAGTTATTTGTTTGT 2040
2041 TACTTCGTCCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGC 2100
2101 TGAGAGGCCTTGGGAGTCATTTATCCCAAACCTGGGTTTTTCTCTCATCCTTCTACCTCC 2160
2161 CTCCTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTT 2220
2221 TTAATTTTGGTTTTTCCTTTTGTATGGGGTTGGGGGAATGGCAGATTTATATGACTT 2280
2281 TTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAA 2340
2341 CACAAGCACAACTAAGTATGTATATACACATGACGCACACGATGCCAGGGCCTAGACCTC 2400
2401 CCAAGGGCTGTGCTCCTGCTCCCAGCAGCCCTCTCTTAGAATATTTAGATGGATGAGCT 2460
2461 TCTGACTCTTTCTTAAAAATTCTTTTGGGAAGATTTCCAGCCTTTCTTCACAACACTTTC 2520
2521 TAACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTATTGTGAAATTAATACCTT 2580
2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640
2641 CAAACATTCTTGTGTAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATG 2700
2701 ACTCCACACTCAGCCTTCTCTACCCTGAAGTGAATTATCACCTTTTCTCCATGTTTCA 2760
2761 GAGTTCTTACTGCCCACAGTTTAAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCT 2820
2821 GTGTTCTGTGTTGTTGTGGAACCTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCC 2880
2881 TTTTGTGTTGTTTAGAGAAAGTTGTATTCACACACAACCTAATAATTTCTTATAAAAAAT 2940
2941 TTTAAACTACAAAGCTACATTTTACTTGCTTGTAGCCGTTTTTGTGTTGCCTTTGGGATT 3000
3001 CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCAATTTTATGATGTCTGTAACA 3060
3061 ACCCAACAAGGTAAGTGAAGCTCCAGAGTTAAGGTTTCAGATTTCTAAATGAACTATCT 3120
3121 TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAACTGTTAATAGCCATCC 3180

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Figure 1D

3181 GTCCATGTAACCTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACA 3240
3241 AGAAGGTAAAAGACCAGTTTTATTTTCAGCATTCCTCATGCATTTTCAGTGGTAACCAAA 3300
3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG 3360
3361 TGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAAAAA 3420
3421 AA 3468

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Figure 2A

1		50
K+betaM2	(1)	-----MALSGNCSRYYPREQSAVPNSFPEVVELNVGGQVYFTRHSTLIS
AAF558201	(1)	-----MPEIIEELNVGGVSYTTLATLLO
CAA20329.1	(1)	-----MTSVEDVITLNVGGTMYTTRSTLSK
Y34129	(1)	-----MDNGDWGYMTDPVTLNVGCHLYTSLTLTR
Y34125	(1)	MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVHIDVGCHMYTSSLATLTK
	51	100
K+betaM2	(46)	IPHSLLWKMFSP--KRDTANDIAKDSKGRFFIDRDGFLFRYILDYLRDRQ
AAF558201	(24)	DKSTLLAEELFG----EGRDSLAKDSKGRYFLDRDGVLFYILDFLRDKA
CAA20329.1	(27)	ETDTLLANIASGSLSEDEQANVVTLPDGTLFVDRDGPLFAYVLHFLRTDK
Y34129	(33)	YPD SMLGAMFGG---D--FPTARDPQGNFYIDRDGPLFRYVLNFLRTSE
Y34125	(51)	YPSRIGRIFDG---T-EPIVLDSLKHQHYFIDRDGQMFYVILNFLRTSK
	101	150
K+betaM2	(94)	VVLPHDFPEKGRLEKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS
AAF558201	(69)	LHLPEGFRERQRLLREAEHFILTAMTECIRSERDAR-----
CAA20329.1	(77)	LSLPEQFREVARLKDEADFYRLERFSTLLSNASSIS-PRPR-----
Y34129	(77)	LTLPLDFKEFDLIRKEADFYQTEPLIQCLNDPKPLY-----
Y34125	(96)	LLTPDDFKDYTLVYEAKEYFQLQPMLEMERWKQDR-----
	151	200
K+betaM2	(144)	QGS DTRICPPSSLLPADRKWGFITVGYRGCTLGREGQADAKFRFVPRIL
AAF558201	(105)	-----PP----GCITVGYRGSFQFGKDGGLADVKFRKLSRIL
CAA20329.1	(117)	-----TANGYNTITSGAETGGYITLGYRGTFAFGRDQADVKFRKLHRIL
Y34129	(113)	-----PMDTFEEVVELSTRKLSKYSNPVAVITQLITTTK
Y34125	(132)	-----ETGRFSRPCECLVVRVAPDLGERITLSCDKSLIEEVE
	201	250
K+betaM2	(194)	VCGRISLAKEVFGETLNESRDPDR-APERYTSRFYLFKFKHLERAFDMLSE
AAF558201	(137)	VCGRVAQCREFVGDTLNESRDPDHGGTDRYTSRFFLKHCIEQAFDNLHD
CAA20329.1	(162)	VCGRATLCREVFADTLNESRDPGG--PDGGE-----
Y34129	(149)	VHSLLEGISNYFTKWNKHMMDDIRD---CQVSFTFGPCDYHQEVSLRVHLM
Y34125	(169)	PEIGDVMCNSVNAGWNHDSDEVIR-----FPLNGYCHLSVQVLERLQQ
	251	300
K+betaM2	(243)	CGEHMVACNSSVTASFIN-----QYTDKIKWSSYTEYVFYREPSRWSPSH
AAF558201	(187)	HGYRMAGSCSGTAGSAAEPKPGVDTEENRWNHYNFVFIRD-----
CAA20329.1	(191)	-----
Y34129	(196)	EYITKQGFTIRNTRVHHMSERANENTVEHNWTFCLARKTDD-----
Y34125	(213)	RGHEIVGSCGGGVDSQFSEYVLRRELARTPRVPSVIRIKQEPPL-----
	301	350
K+betaM2	(288)	CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQT
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----
	351	400
K+betaM2	(338)	NIQTLDRPIKKGVPQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKE
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----

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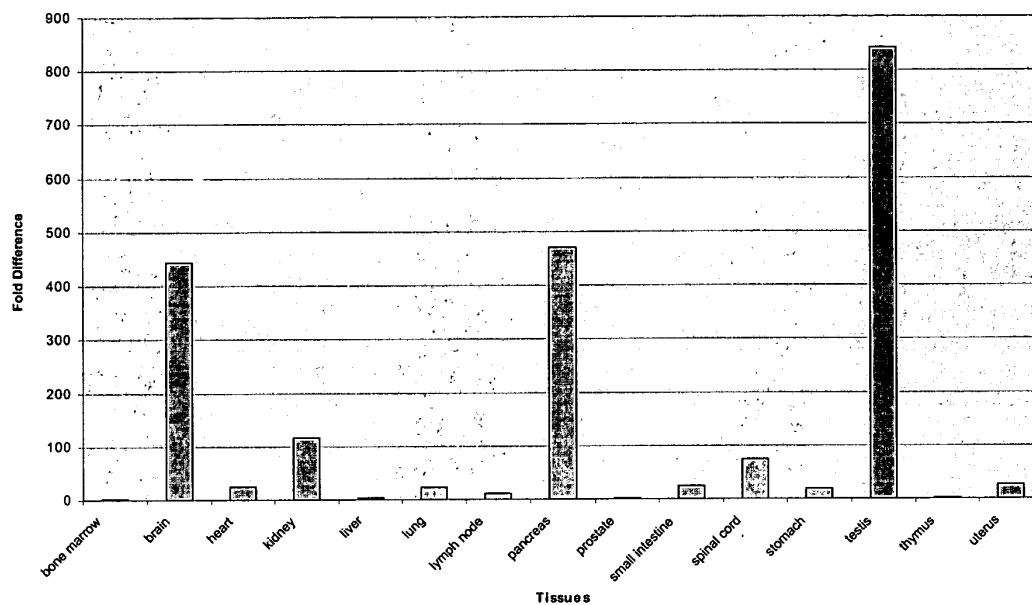
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Figure 2B

		401	441
K+betaM2	(388)	KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL	
AAF558201	(229)	-----	
CAA20329.1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	
Consensus	(401)		

10056834.012402
204270.433500

Figure 3



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Figure 4.

Protein	Genbank ID	Identities	Similarities
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

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Figure 5

